

SEQUENCE LISTING

<110> MARINE BIOTECHNOLOGY INSTITUTE CO., LTD.

<120> A NOVEL CAROTENOID HYDROXYLASE GENE AND A METHOD FOR PRODUCING HYDROXY CAROTENOID AND A NOVEL GERANYLGERANYLPYROPHOSPHATE SYNTHETASE GENE

<130> FP-042PCT

<150> JP 2003/388165

<151> 2003-11-26

<150> JP 2004/165919

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tcggccatctg cagttatggac gacgaggcca gacgtcccc gccgctcatg gcgatgaccc	11618
gcaggaggatc cctcaaatgc cgggtgtcca tcatgaagtt cagcccgatcg cggccggca	11678
tcagaatgtc caccagcact gcgtcggcg accagtccctc gacgatccgc aaccgcgtgt	11738
tgaccgttgc tgcggtcagg acttggcaac ccagccgttt cagcatctcc tccagatgaa	11798

gcagaaccag cgaatcgcc tcgatcacgc agactttcac gcccaacctc cagatgcgat 11858
 cagggggAAC taacggatga atccatgtt gcgtcaactc ggaagacggc gttccgact 11918
 ggccatcgcc ttggcgggcg cggcgtgac cctgcttctg gcggccactg gggtgacgct 11978
 gcaacgagaa ttc 11991

<210> 3
 <211> 774
 <212> DNA
 <213> Brevundimonas sp.

<220>
 <221> CDS
 <222> (1).. (771)

<400> 3

atg	ttg	agg	gat	ctg	ctc	atc	acc	acc	ctg	gcg	ctg	agc	ctg	atc	atc	48
Met	Leu	Arg	Asp	Leu	Leu	Ile	Thr	Thr	Leu	Ala	Leu	Ser	Leu	Ile	Ile	
1	5					10								15		

ggc	ctg	cgc	tat	ctg	ctg	gtc	ggc	gcg	gcf	gcc	cat	ggg	ctg	ctg	tgg	96
Gly	Leu	Arg	Tyr	Leu	Leu	Val	Gly	Ala	Ala	Ala	Ala	His	Gly	Leu	Leu	Trp
20						25							30			

gcc	ggg	gcf	ggc	cgg	gga	cgg	gcf	ctg	aat	ctg	cgg	ccg	ccg	gcf	atg	144	
Ala	Gly	Ala	Gly	Arg	Gly	Arg	Gly	Arg	Ala	Leu	Asn	Leu	Arg	Pro	Pro	Ala	Met
35						40								45			

aag	cgc	atc	cgc	gcc	gag	atc	gtc	gcc	tcc	ctg	atc	gcc	tgc	ccc	atc	192
Lys	Arg	Ile	Arg	Ala	Glu	Ile	Val	Ala	Ser	Leu	Ile	Ala	Cys	Pro	Ile	
50					55					60						

tac	gcc	ctg	ccg	gcf	gcc	ctg	gtg	ctg	gag	ctg	tgg	aag	cgg	ggc	ggg	240
Tyr	Ala	Leu	Pro	Ala	Ala	Leu	Val	Leu	Glu	Leu	Trp	Lys	Arg	Gly	Gly	
65					70			75			80					

acg	gcf	atc	tac	agc	gat	ccc	gac	gcc	tgg	ccc	ctg	tgg	tgg	ctg	ccg	288
Thr	Ala	Ile	Tyr	Ser	Asp	Pro	Asp	Ala	Trp	Pro	Leu	Trp	Trp	Leu	Pro	
85					90						95					

gtc	agt	ctg	atc	gtc	tat	ctg	ctg	gcf	cac	gac	gcc	ttc	tac	tac	tgg	336
Val	Ser	Leu	Ile	Val	Tyr	Leu	Leu	Ala	His	Asp	Ala	Phe	Tyr	Tyr	Trp	
100						105							110			

gtg cac agg gcc ctg cat cac ccg cgc gtc ttc ggc tgg gcc cat gcc	384		
Val His Arg Ala Leu His His Pro Arg Val Phe Gly Trp Ala His Ala			
115	120	125	
gaa cac cac cgg tcg cgc gac ccc agc gcc ttc gcc tcc ttc gcc ttc	432		
Glu His His Arg Ser Arg Asp Pro Ser Ala Phe Ala Ser Phe Ala Phe			
130	135	140	
gac ccg gcc gag gct gcg gcc acc gcc tgg ttc ctg ccc gcc ctg gcc	480		
Asp Pro Ala Glu Ala Ala Ala Thr Ala Trp Phe Leu Pro Ala Leu Ala			
145	150	155	160
ctg atc gtg ccg atc cac tgg ggc gtg gcc ctg acc ctg ctg acg ctg	528		
Leu Ile Val Pro Ile His Trp Gly Val Ala Leu Thr Leu Leu Thr Leu			
165	170	175	
atg tcg ctg acg gcc ctg aac cat gcg ggg cgc gag gtc tgg ccc	576		
Met Ser Leu Thr Ala Ala Leu Asn His Ala Gly Arg Glu Val Trp Pro			
180	185	190	
gcc gcc tgg ctg gag cgg gcg ctt cgc tgg ctg atc acc gcc acc	624		
Ala Ala Trp Leu Glu Arg Ala Pro Leu Arg Trp Leu Ile Thr Ala Thr			
195	200	205	
cac cac gac gcc cac cac aag cgg ttc aac gga aac tac ggc ctc tat	672		
His His Asp Ala His His Lys Arg Phe Asn Gly Asn Tyr Gly Leu Tyr			
210	215	220	
ttc cag ttc tgg gac cgc tgg gcc ggg act gag gtt tcg gcc gcc ccc	720		
Phe Gln Phe Trp Asp Arg Trp Ala Gly Thr Glu Val Ser Ala Ala Pro			
225	230	235	240
tcg cca cca tcc ccg gtc atc cct cca gag cgg ccc tca gcg cct ctt	768		
Ser Pro Pro Ser Pro Val Ile Pro Pro Glu Arg Pro Ser Ala Pro Leu			
245	250	255	
cggtga	774		
Arg			

<210> 4
 <211> 257
 <212> PRT
 <213> Brevundimonas sp.

<400> 4
 Met Leu Arg Asp Leu Leu Ile Thr Thr Leu Ala Leu Ser Leu Ile Ile
 1 5 10 15

Gly Leu Arg Tyr Leu Leu Val Gly Ala Ala Ala His Gly Leu Leu Trp
 20 25 30

Ala Gly Ala Gly Arg Gly Arg Ala Leu Asn Leu Arg Pro Pro Ala Met
 35 40 45

Lys Arg Ile Arg Ala Glu Ile Val Ala Ser Leu Ile Ala Cys Pro Ile
 50 55 60

Tyr Ala Leu Pro Ala Ala Leu Val Leu Glu Leu Trp Lys Arg Gly Gly
 65 70 75 80

Thr Ala Ile Tyr Ser Asp Pro Asp Ala Trp Pro Leu Trp Trp Leu Pro
 85 90 95

Val Ser Leu Ile Val Tyr Leu Leu Ala His Asp Ala Phe Tyr Tyr Trp
 100 105 110

Val His Arg Ala Leu His His Pro Arg Val Phe Gly Trp Ala His Ala
 115 120 125

Glu His His Arg Ser Arg Asp Pro Ser Ala Phe Ala Ser Phe Ala Phe
 130 135 140

Asp Pro Ala Glu Ala Ala Ala Thr Ala Trp Phe Leu Pro Ala Leu Ala
 145 150 155 160

Leu Ile Val Pro Ile His Trp Gly Val Ala Leu Thr Leu Leu Thr Leu
 165 170 175

Met Ser Leu Thr Ala Ala Leu Asn His Ala Gly Arg Glu Val Trp Pro
 180 185 190

Ala Ala Trp Leu Glu Arg Ala Pro Leu Arg Trp Leu Ile Thr Ala Thr
 195 200 205

His His Asp Ala His His Lys Arg Phe Asn Gly Asn Tyr Gly Leu Tyr
 210 215 220

Phe Gln Phe Trp Asp Arg Trp Ala Gly Thr Glu Val Ser Ala Ala Pro
 225 230 235 240

Ser Pro Pro Ser Pro Val Ile Pro Pro Glu Arg Pro Ser Ala Pro Leu
 245 250 255

Arg

<210> 5
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 5
tacgaattcg atgcccctcg ccctg 25

<210> 6
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 6
tagaggatcc tcaaggatgc aactggatcg ta 32

<210> 7
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 7
tacgaattcg atgaccggccg ccgtcg 26

<210> 8
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 8

tagaggatcc tcaagactcg ccgcgcaca a

31

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 9
tacgaattcg ctgtcgccga tgcaggc

27

<210> 10
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 10
tagaggatcc tgcgggttcag cagccgataa aa

32

<210> 11
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 11
tacgaattcg atgcgagcag cagtgtatcg a

31

<210> 12
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 12

tagaggatcc aagctcttgg agccctgct 29

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 13
tacgaattcg atgagcgcacg ccgtcct 27

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 14
tagaggatcc tcagatgtgg gtccacagg 29

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 15
tacgaattcg atgatggcgg tggcggc 28

<210> 16
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 16

tagaggatcc cccacatctg acggcgct

28

<210> 17
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 17
tacgaattcg atgtccttca tctcttccgg c

31

<210> 18
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 18
tagaggatcc accgccatca tgacgagg

28

<210> 19
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 19
tacgaattcg atggcgatcg tcggctaa

29

<210> 20
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 20

tagaggatcc ctagcgtcca agttcggcct 30

<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 21
tacgaattcg atgcccaccc ccgacgacg 29

<210> 22
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 22
tagaggatcc tcagaagcgg ggctcttcca 30

<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 23
tacgaattcg atggcctggc tgacgtggat 30

<210> 24
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 24

tagaggatcc tcaggcgccg ctgctggaa 29

<210> 25
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 25
tacgaattcg atgttggagg atctgctcat ca 32

<210> 26
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 26
tagaggatcc tcaccgaaga ggcgcgtgag 29

<210> 27
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 27
tacgaattcg atgctgaaac ggctgggtt 29

<210> 28
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 28

tagaggatcc ctatccat ttctggacc g

31

<210> 29
 <211> 486
 <212> DNA
 <213> Brevundimonas sp.

<220>
 <221> CDS
 <222> (1).. (483)

<400> 1

atg gcc tgg ctg acg tgg atc gcg ctg ttc ctg acc gcc ttt ttg ggc 48
 Met Ala Trp Leu Thr Trp Ile Ala Leu Phe Leu Thr Ala Phe Leu Gly
 1 5 10 15

atg gag gcg ttc gcc tgg atc atg cac cgc tat gtg atg cac ggt ttc 96
 Met Glu Ala Phe Ala Trp Ile Met His Arg Tyr Val Met His Gly Phe
 20 25 30

ctg tgg tcc tgg cac cgc agc cat cat gag ccg cac gat cac ccc ctg 144
 Leu Trp Ser Trp His Arg Ser His His Glu Pro His Asp His Pro Leu
 35 40 45

gag aag aac gac ctg ttc gcc gtg gtc ttc gcc gcc ccg gcc atc gtc 192
 Glu Lys Asn Asp Leu Phe Ala Val Val Phe Ala Ala Pro Ala Ile Val
 50 55 60

atg gtg gcc gtg ggt ctg cac ctg tgg ccc tgg gcc ctg ccg gtc ggc 240
 Met Val Ala Val Gly Leu His Leu Trp Pro Trp Ala Leu Pro Val Gly
 65 70 75 80

ctg ggg atc acg gcc tat ggg atg gtc tat ttc ttc ttc cac gac ggc 288
 Leu Gly Ile Thr Ala Tyr Gly Met Val Tyr Phe Phe Phe His Asp Gly
 85 90 95

ctg gtg cac cgg cgg ttc ccg acg ggc ttt tcc ggg cgg tcc ggc ttc 336
 Leu Val His Arg Arg Phe Pro Thr Gly Phe Ser Gly Arg Ser Gly Phe
 100 105 110

tgg acg cgg cgc atc cag gcg cac cgt ctg cat cac gcc gtg cgc acg 384
 Trp Thr Arg Arg Ile Gln Ala His Arg Leu His His Ala Val Arg Thr
 115 120 125

cgc gaa ggc tgc tcc ttc ggc ttt ctg tgg gtg cgg tcg gcg cgg 432
 Arg Glu Gly Cys Val Ser Phe Gly Phe Leu Trp Val Arg Ser Ala Arg
 130 135 140

gca ctg aag gcc gaa ctg gct cag aag cgg ggc tct tcc agc agc ggc 480
 Ala Leu Lys Ala Glu Leu Ala Gln Lys Arg Gly Ser Ser Ser Ser Gly
 145 150 155 160

gcc tga 486
 Ala

<210> 30
 <211> 161
 <212> PRT
 <213> Brevundimonas sp.

<400> 30
 Met Ala Trp Leu Thr Trp Ile Ala Leu Phe Leu Thr Ala Phe Leu Gly
 1 5 10 15

Met Glu Ala Phe Ala Trp Ile Met His Arg Tyr Val Met His Gly Phe
 20 25 30

Leu Trp Ser Trp His Arg Ser His His Glu Pro His Asp His Pro Leu
 35 40 45

Glu Lys Asn Asp Leu Phe Ala Val Val Phe Ala Ala Pro Ala Ile Val
 50 55 60

Met Val Ala Val Gly Leu His Leu Trp Pro Trp Ala Leu Pro Val Gly
 65 70 75 80

Leu Gly Ile Thr Ala Tyr Gly Met Val Tyr Phe Phe Phe His Asp Gly
 85 90 95

Leu Val His Arg Arg Phe Pro Thr Gly Phe Ser Gly Arg Ser Gly Phe
 100 105 110

Trp Thr Arg Arg Ile Gln Ala His Arg Leu His His Ala Val Arg Thr
 115 120 125

Arg Glu Gly Cys Val Ser Phe Gly Phe Leu Trp Val Arg Ser Ala Arg
 130 135 140

Ala Leu Lys Ala Glu Leu Ala Gln Lys Arg Gly Ser Ser Ser Ser Gly
 145 150 155 160

Ala

<210> 31
 <211> 897
 <212> DNA
 <213> Brevundimonas sp.

<220>
 <221> CDS
 <222> (1).. (894)

<400> 31

atg	gct	atc	gtc	ggc	tta	agg	ccc	cag	ccc	gtg	tcg	gac	ccc	gaa	cct	48
Met																
Ala	Ile	Val	Gly	Leu	Arg	Pro	Gln	Pro	Val	Ser	Asp	Pro	Glu	Pro		
1	5	10													15	

cag	tcg	ccc	gag	aat	ctg	cgt	ggc	ctg	gtg	cag	gac	cgg	ctg	gcc	gag	96
Gln																
Ser	Pro	Glu	Asn	Leu	Arg	Gly	Leu	Val	Gln	Asp	Arg	Leu	Ala	Glu		
20															30	

acg	gct	ccc	tca	tgc	gac	ggt	ctt	tta	gcc	ctc	gcc	gct	cgc	gag	gcc	144
Thr																
Ala	Pro	Ser	Ser	Asp	Gly	Leu	Leu	Ala	Leu	Ala	Ala	Arg	Glu	Ala		
35															45	

ctg	ctg	gga	ccg	ggc	aag	cg	gtc	agg	ccg	gtc	gtg	gcc	atg	ttg	gcc	192
Leu	Leu	Gly	Pro	Gly	Lys	Arg	Val	Arg	Pro	Val	Val	Ala	Met	Leu	Ala	
50															60	

gcc	gct	cac	gtc	ggc	ggg	ccg	gcc	gag	gac	gcc	ctg	gat	ttc	ggt	tgc	240
Ala	Ala	His	Val	Gly	Gly	Arg	Ala	Glu	Asp	Ala	Leu	Asp	Phe	Gly	Cys	
65															80	

gct	gtc	gaa	atg	gcc	cat	gcc	gcc	tcc	ctg	gtt	ctg	gac	gac	ctg	ccc	288
Ala	Val	Glu	Met	Ala	His	Ala	Ala	Ser	Leu	Val	Leu	Asp	Asp	Leu	Pro	
85															95	

tgt	atg	gat	gat	gct	ttg	cg	cg	ggt	cag	cg	acc	ctg	cac	cg	336	
Cys																
Met	Asp	Asp	Ala	Ala	Leu	Arg	Arg	Gly	Gln	Pro	Thr	Leu	His	Arg		
100															110	

cg	cac	ggc	gag	gat	gct	gtc	gtc	gct	gtc	ttt	ttt	ttt	ttt	ttt	ttt	384
Arg	His	Gly	Glu	Asp	Ala	Ala	Val	Leu	Ala	Ala	Val	Ala	Leu	Leu	Asn	
115															125	

caa	tcg	acc	cg	ctg	att	ctg	caa	agc	cg	gct	tcg	gag	gct	cg	432	
Gln	Ser	Thr	Arg	Leu	Ile	Leu	Gln	Ser	Arg	Ala	Pro	Ser	Glu	Ala	Arg	
130															140	

ctg	ggc	gcc	ctg	gac	gat	ttt	acg	cag	gct	atc	ggc	ttt	gac	ggc	ctg	480
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Leu	Gly	Ala	Leu	Asp	Asp	Leu	Thr	Gln	Ala	Ile	Gly	Phe	Asp	Gly	Leu
145						150					155				160
gcc gag ggc cag atg cgc gat ctg cgc gac gat ccc gtt cag cgc gac															528
Ala	Glu	Gly	Gln	Met	Arg	Asp	Leu	Arg	Asp	Asp	Pro	Val	Gln	Arg	Asp
						165					170				175
gtg gtc gcc ctg cgt cgg atc aac gat ctg aag acc ggc gcc ctg ttc															576
Val	Val	Ala	Leu	Arg	Arg	Ile	Asn	Asp	Leu	Lys	Thr	Gly	Ala	Leu	Phe
						180					185				190
gtc gcg gcc gcg cgg ggc ggc ggc cgg atg ggc ggc ggc gat gcg gac															624
Val	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Met	Gly	Gly	Gly	Asp	Ala	Asp	
						195					200				205
gac ctg gcg cgt ctc gcc gcc ttc ggc gaa gcg gtc ggc ttc gcc ttc															672
Asp	Leu	Ala	Arg	Leu	Ala	Ala	Phe	Gly	Glu	Ala	Val	Gly	Phe	Ala	Phe
						210					215				220
cag ctt tgc gac gac ctg atg gac gcc tgt tcg acg agc gag gcc ttg															720
Gln	Leu	Cys	Asp	Asp	Leu	Met	Asp	Ala	Cys	Ser	Thr	Glu	Ala	Leu	
						225					230				235
ggc aag gac gtg ggt cag gat cag ggc gtg acc acc ttc gtg gac ctg															768
Gly	Lys	Asp	Val	Gly	Gln	Asp	Gln	Gly	Val	Thr	Thr	Phe	Val	Asp	Leu
						245					250				255
tgg ggc gaa ggc cgg gtc cgc gcc ggg gtg cgc cag tca ctg gcc cgg															816
Trp	Gly	Glu	Gly	Arg	Val	Arg	Ala	Gly	Val	Arg	Gln	Ser	Leu	Ala	Arg
						260					265				270
gcg gcc gag gcg gtc ggg cac gac agc ccc ctg acg acc tat gtc ctt															864
Ala	Ala	Glu	Ala	Val	Gly	His	Asp	Ser	Pro	Leu	Thr	Thr	Tyr	Val	Leu
						275					280				285
cat ctc ttc cgg cag gcc gaa ctt gga cgc tag															897
His	Leu	Phe	Arg	Gln	Ala	Glu	Leu	Gly	Arg						
						290					295				
<210> 32															
<211> 298															
<212> PRT															
<213> Brevundimonas sp.															
<400> 32															
Met	Ala	Ile	Val	Gly	Leu	Arg	Pro	Gln	Pro	Val	Ser	Asp	Pro	Glu	Pro
1			5							10					15

Gln Ser Pro Glu Asn Leu Arg Gly Leu Val Gln Asp Arg Leu Ala Glu
 20 25 30

Thr Ala Pro Ser Ser Asp Gly Leu Leu Ala Leu Ala Ala Arg Glu Ala
 35 40 45

Leu Leu Gly Pro Gly Lys Arg Val Arg Pro Val Val Ala Met Leu Ala
 50 55 60

Ala Ala His Val Gly Gly Arg Ala Glu Asp Ala Leu Asp Phe Gly Cys
 65 70 75 80

Ala Val Glu Met Ala His Ala Ala Ser Leu Val Leu Asp Asp Leu Pro
 85 90 95

Cys Met Asp Asp Ala Ala Leu Arg Arg Gly Gln Pro Thr Leu His Arg
 100 105 110

Arg His Gly Glu Asp Ala Ala Val Leu Ala Ala Val Ala Leu Leu Asn
 115 120 125

Gln Ser Thr Arg Leu Ile Leu Gln Ser Arg Ala Pro Ser Glu Ala Arg
 130 135 140

Leu Gly Ala Leu Asp Asp Leu Thr Gln Ala Ile Gly Phe Asp Gly Leu
 145 150 155 160

Ala Glu Gly Gln Met Arg Asp Leu Arg Asp Asp Pro Val Gln Arg Asp
 165 170 175

Val Val Ala Leu Arg Arg Ile Asn Asp Leu Lys Thr Gly Ala Leu Phe
 180 185 190

Val Ala Ala Ala Arg Gly Gly Arg Met Gly Gly Asp Ala Asp
 195 200 205

Asp Leu Ala Arg Leu Ala Ala Phe Gly Glu Ala Val Gly Phe Ala Phe
 210 215 220

Gln Leu Cys Asp Asp Leu Met Asp Ala Cys Ser Thr Ser Glu Ala Leu
 225 230 235 240

Gly Lys Asp Val Gly Gln Asp Gln Gly Val Thr Thr Phe Val Asp Leu
 245 250 255

Trp Gly Glu Gly Arg Val Arg Ala Gly Val Arg Gln Ser Leu Ala Arg
 260 265 270

Ala Ala Glu Ala Val Gly His Asp Ser Pro Leu Thr Thr Tyr Val Leu
275 280 285

His Leu Phe Arg Gln Ala Glu Leu Gly Arg
290 295